

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Use of a gene for increase of oil content in plants

<130> 437-02

<140> 53702

<141> 2002-07-10

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 2439

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (30)..(1994)

<400> 1

```

ctt gtagagg ttaactgggg agtattaca atg atg gca act ccg gct act gat 53
                                Met Met Ala Thr Pro Ala Thr Asp
                                1                               5

ctt att tcc gat aat gat aaa tat aac aag caa tgt ctt tct gat tca 101
Leu Ile Ser Asp Asn Asp Lys Tyr Asn Lys Gln Cys Leu Ser Asp Ser
    10                      15                      20

agt gat agt ggt agt gat gta agc ttt ttt tcc gta aat gaa agc gaa 149
Ser Asp Ser Gly Ser Asp Val Ser Phe Phe Ser Val Asn Glu Ser Glu
    25                      30                      35                      40

ggt gaa ttg gat aca atg gag aaa gtg gat acc ttg att gga ggt gca 197
Gly Glu Leu Asp Thr Met Glu Lys Val Asp Thr Leu Ile Gly Gly Ala
                      45                      50                      55

aga gtt ata agc aat aaa gta gaa aaa gac agc gat agt gaa caa agg 245
Arg Val Ile Ser Asn Lys Val Glu Lys Asp Ser Asp Ser Glu Gln Arg
                      60                      65                      70

gga aga aag aag gaa aca act ggg ccc aat aac tat cat aat tta gaa 293
Gly Arg Lys Lys Glu Thr Thr Gly Pro Asn Asn Tyr His Asn Leu Glu
                      75                      80                      85

gag aag caa gcg agt gcc att tct ctt gac gct gat gat gaa gat ctc 341
Glu Lys Gln Ala Ser Ala Ile Ser Leu Asp Ala Asp Asp Glu Asp Leu
    90                      95                      100

gat gaa att att tct tat tcg cat gac ggg aac tat gac agc tct cat 389
Asp Glu Ile Ile Ser Tyr Ser His Asp Gly Asn Tyr Asp Ser Ser His
105                      110                      115                      120

```

aaa act ttc tcc ttt tcc tta cca ttt ggt aat aca aat ttc cga tca	437
Lys Thr Phe Ser Phe Ser Leu Pro Phe Gly Asn Thr Asn Phe Arg Ser	
125 130 135	
agt tca cca tta gcc ata att aaa act gtg ctt ccc aag act cca gat	485
Ser Ser Pro Leu Ala Ile Ile Lys Thr Val Leu Pro Lys Thr Pro Asp	
140 145 150	
gag ttc atc aaa aag aat cta aga aag aat gag atc aag caa aaa ctg	533
Glu Phe Ile Lys Lys Asn Leu Arg Lys Asn Glu Ile Lys Gln Lys Leu	
155 160 165	
aaa aaa tca acc tcc att tct tcc ttg gaa gag ata gaa tta ttt aaa	581
Lys Lys Ser Thr Ser Ile Ser Ser Leu Glu Glu Ile Glu Leu Phe Lys	
170 175 180	
tac gaa agg ggc att gat aat tca agg tta agg gct gtt aaa gaa tct	629
Tyr Glu Arg Gly Ile Asp Asn Ser Arg Leu Arg Ala Val Lys Glu Ser	
185 190 195 200	
ttg gaa atg gat gcc ttg aag aac tcc att aag caa ata aca gca gac	677
Leu Glu Met Asp Ala Leu Lys Asn Ser Ile Lys Gln Ile Thr Ala Asp	
205 210 215	
cca ttc gac aaa act cat gac gga tat tac cgt tcg cgt tta gaa tct	725
Pro Phe Asp Lys Thr His Asp Gly Tyr Tyr Arg Ser Arg Leu Glu Ser	
220 225 230	
ata tgg aat gaa ttg gaa gga gat gtc gtt ata atg ggt gga tat cga	773
Ile Trp Asn Glu Leu Glu Gly Asp Val Val Ile Met Gly Gly Tyr Arg	
235 240 245	
ggt agt gtg cta agg gat gct act act cat aag cga att tgg atc cca	821
Gly Ser Val Leu Arg Asp Ala Thr Thr His Lys Arg Ile Trp Ile Pro	
250 255 260	
tta aag gca ggt ttg aat atg acg aaa gtc gat tta ttg atc gga cct	869
Leu Lys Ala Gly Leu Asn Met Thr Lys Val Asp Leu Leu Ile Gly Pro	
265 270 275 280	
aat gac gaa gat gaa ctt aaa act cag aag gag att gtc cct gat gga	917
Asn Asp Glu Asp Glu Leu Lys Thr Gln Lys Glu Ile Val Pro Asp Gly	
285 290 295	
atg cta aca cat ata ggg cct gtt gat atc tct aag agg ttg ata aag	965
Met Leu Thr His Ile Gly Pro Val Asp Ile Ser Lys Arg Leu Ile Lys	
300 305 310	
agg cta gac gca aat cct aat tta aat gtt cag cag ttt ggc tat gat	1013
Arg Leu Asp Ala Asn Pro Asn Leu Asn Val Gln Gln Phe Gly Tyr Asp	
315 320 325	
tgg aga tta tcc ttg gac ata tct gcc aag cat tta acg act aaa cta	1061
Trp Arg Leu Ser Leu Asp Ile Ser Ala Lys His Leu Thr Thr Lys Leu	
330 335 340	
gag gaa att tac aat aag caa aaa aat aag aag gga ata tac atc att	1109

Glu 345	Glu	Ile	Tyr	Asn 350	Lys	Gln	Lys	Asn	Lys	Lys 355	Gly	Ile	Tyr	Ile	Ile 360	
gcc Ala	cat His	tca Ser	atg Met	ggc Gly 365	gga Gly	ttg Leu	gtc Val	gca Ala	cat His	aaa Lys 370	gtg Val	ttg Leu	caa Gln	gac Asp 375	tgt Cys	1157
act Thr	cat His	ttg Leu	ata Ile 380	aga Arg	ggc Gly	att Ile	att Ile	tac Tyr 385	gtg Val	ggc Gly	tcc Ser	cca Pro	agc Ser	caa Gln	tgt Cys	1205
cca Pro	aat Asn	att Ile 395	tta Leu	ggc Gly	cct Pro	att Ile	agg Arg	ttt Phe 400	gga Gly	gat Asp	gat Asp	gtg Val	atg Met	tgg Trp	aat Asn	1253
aaa Lys 410	cta Leu	ttt Phe	tca Ser	cta Leu	aga Arg	acc Thr 415	aac Asn	ttt Phe	ttt Phe	atg Met	aga Arg	agt Ser	agt Ser	ttc Phe	tat Tyr	1301
ttt Phe 425	cta Leu	ccg Pro	tta Leu	gat Asp	ggc Gly 430	aga Arg	tgt Cys	ttt Phe	gtt Val	gac Asp 435	aaa Lys	att Ile	acc Thr	tta Leu	gag Glu 440	1349
agg Arg	tat Tyr	gat Asp	ttc Phe 445	gat Asp	ttt Phe	ttt Phe	gat Asp	aca Thr	gat Asp	gtt Val	tgg Trp	aaa Lys	acc Thr	ctt Leu	ggc Gly 455	1397
ttg Leu	tca Ser	cct Pro	ctc Leu	gtc Val	aat Asn	gag Glu	aaa Lys	aga Arg	gag Glu	gaa Glu	tca Ser	gct Ala	cac His	gaa Glu	aaa Lys	1445
tca Ser	aaa Lys	tta Leu	tta Leu	cca Pro	agg Arg	aaa Lys	acg Thr	aaa Lys	tca Ser	gcg Ala	ctt Leu	tcg Ser	ctt Leu	aaa Lys	gct Ala	1493
acc Thr	cta Leu	aac Asn	gca Ala	act Thr	acc Thr	aag Lys	ttt Phe	gtc Val	cta Leu	aat Asn	gca Ala	cct Pro	gtt Val	gtt Val	agg Arg	1541
aat Asn 505	gta Val	gcc Ala	ggc Gly	aat Asn	aat Asn	aaa Lys	cag Gln	gta Val	cca Pro	agg Arg	gat Asp	gtg Val	cct Pro	ttc Phe	gat Asp 520	1589
gaa Glu	gtc Val	ttc Phe	cat His	aca Thr	tct Ser	tat Tyr	gaa Glu	gat Asp	agc Ser	tgt Cys	gaa Glu	tat Tyr	tta Leu	gcg Ala	aga Arg	1637
act Thr	tta Leu	aaa Lys	cgt Arg	aca Thr	aag Lys	aat Asn	tat Tyr	ttg Leu	gat Asp	agc Ser	tta Leu	gat Asp	tac Tyr	gac Asp	ccg Pro	1685
aac Asn	aaa Lys	gaa Glu	tat Tyr	cct Pro	cca Pro	ttg Leu	gcc Ala	atg Met	gtt Val	tac Tyr	ggc Gly	aac Asn	aag Lys	gtt Val	ccc Pro	1733
act Thr	gtt Val	aga Arg	ggc Gly	gct Ala	aaa Lys	gtg Val	aac Asn	ggc Gly	ata Ile	caa Gln	gat Asp	ata Ile	aaa Lys	gat Asp	ggg Gly	1781

570

575

580

aat tat gaa gat ttt tac tat ggt ccg ggc gac ggt gtt gtt cac cat 1829
 Asn Tyr Glu Asp Phe Tyr Tyr Gly Pro Gly Asp Gly Val Val His His
 585 590 595 600

aaa tgg tta ttg cct gaa cag aga ggc ttt cca gtt gtt tgt aaa atc 1877
 Lys Trp Leu Leu Pro Glu Gln Arg Gly Phe Pro Val Val Cys Lys Ile
 605 610 615

gcc agt tct tca ggt cat gtt agc tta atg acg gat ttg aaa tca atg 1925
 Ala Ser Ser Ser Gly His Val Ser Leu Met Thr Asp Leu Lys Ser Met
 620 625 630

gca aaa gca ttc ata tct atc gtc gac agc gaa aaa gaa gga aga aga 1973
 Ala Lys Ala Phe Ile Ser Ile Val Asp Ser Glu Lys Glu Gly Arg Arg
 635 640 645

tct cga aca cga act tct tca tgaaaggcctt tttattcctt tgtttactat 2024
 Ser Arg Thr Arg Thr Ser Ser
 650 655

tcatatctgc atttttcttt ttacccaaat tccgcatgtc aaaaaaatc tggcaacgca 2084

ccgcgaataa aaataaataa tatttttttta tcttttagttg cctaaatact atttatttcg 2144

tcaattttac aacctctttt atatacacca ttcgatttcc cacgaagtaa aataataatt 2204

ctataaacag atttatctga tatgctcaat ttccctccc attttcatta ttgtccttct 2264

tgctcttctc cgatgtcaaa attaaccttc agccataagc tgcattgctt acattggggtt 2324

aataattgat aaccagaatg actccgttcc atagcgtcta cattatcaat gcattcatct 2384

aacaaactct cactaaaatg aaaaccacca acaaattgac agcgaggaca attca 2439

<210> 2

<211> 655

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

Met Met Ala Thr Pro Ala Thr Asp Leu Ile Ser Asp Asn Asp Lys Tyr
 1 5 10 15

Asn Lys Gln Cys Leu Ser Asp Ser Ser Asp Ser Gly Ser Asp Val Ser
 20 25 30

Phe Phe Ser Val Asn Glu Ser Glu Gly Glu Leu Asp Thr Met Glu Lys
 35 40 45

Val Asp Thr Leu Ile Gly Gly Ala Arg Val Ile Ser Asn Lys Val Glu
 50 55 60

Lys Asp Ser Asp Ser Glu Gln Arg Gly Arg Lys Lys Glu Thr Thr Gly
 65 70 75 80

Pro Asn Asn Tyr His Asn Leu Glu Glu Lys Gln Ala Ser Ala Ile Ser
 85 90 95
 Leu Asp Ala Asp Asp Glu Asp Leu Asp Glu Ile Ile Ser Tyr Ser His
 100 105 110
 Asp Gly Asn Tyr Asp Ser Ser His Lys Thr Phe Ser Phe Ser Leu Pro
 115 120 125
 Phe Gly Asn Thr Asn Phe Arg Ser Ser Ser Pro Leu Ala Ile Ile Lys
 130 135 140
 Thr Val Leu Pro Lys Thr Pro Asp Glu Phe Ile Lys Lys Asn Leu Arg
 145 150 155 160
 Lys Asn Glu Ile Lys Gln Lys Leu Lys Lys Ser Thr Ser Ile Ser Ser
 165 170 175
 Leu Glu Glu Ile Glu Leu Phe Lys Tyr Glu Arg Gly Ile Asp Asn Ser
 180 185 190
 Arg Leu Arg Ala Val Lys Glu Ser Leu Glu Met Asp Ala Leu Lys Asn
 195 200 205
 Ser Ile Lys Gln Ile Thr Ala Asp Pro Phe Asp Lys Thr His Asp Gly
 210 215 220
 Tyr Tyr Arg Ser Arg Leu Glu Ser Ile Trp Asn Glu Leu Glu Gly Asp
 225 230 235 240
 Val Val Ile Met Gly Gly Tyr Arg Gly Ser Val Leu Arg Asp Ala Thr
 245 250 255
 Thr His Lys Arg Ile Trp Ile Pro Leu Lys Ala Gly Leu Asn Met Thr
 260 265 270
 Lys Val Asp Leu Leu Ile Gly Pro Asn Asp Glu Asp Glu Leu Lys Thr
 275 280 285
 Gln Lys Glu Ile Val Pro Asp Gly Met Leu Thr His Ile Gly Pro Val
 290 295 300
 Asp Ile Ser Lys Arg Leu Ile Lys Arg Leu Asp Ala Asn Pro Asn Leu
 305 310 315 320
 Asn Val Gln Gln Phe Gly Tyr Asp Trp Arg Leu Ser Leu Asp Ile Ser
 325 330 335
 Ala Lys His Leu Thr Thr Lys Leu Glu Glu Ile Tyr Asn Lys Gln Lys
 340 345 350
 Asn Lys Lys Gly Ile Tyr Ile Ile Ala His Ser Met Gly Gly Leu Val
 355 360 365
 Ala His Lys Val Leu Gln Asp Cys Thr His Leu Ile Arg Gly Ile Ile
 370 375 380

Tyr Val Gly Ser Pro Ser Gln Cys Pro Asn Ile Leu Gly Pro Ile Arg
 385 390 395 400
 Phe Gly Asp Asp Val Met Trp Asn Lys Leu Phe Ser Leu Arg Thr Asn
 405 410 415
 Phe Phe Met Arg Ser Ser Phe Tyr Phe Leu Pro Leu Asp Gly Arg Cys
 420 425 430
 Phe Val Asp Lys Ile Thr Leu Glu Arg Tyr Asp Phe Asp Phe Phe Asp
 435 440 445
 Thr Asp Val Trp Lys Thr Leu Gly Leu Ser Pro Leu Val Asn Glu Lys
 450 455 460
 Arg Glu Glu Ser Ala His Glu Lys Ser Lys Leu Leu Pro Arg Lys Thr
 465 470 475 480
 Lys Ser Ala Leu Ser Leu Lys Ala Thr Leu Asn Ala Thr Thr Lys Phe
 485 490 495
 Val Leu Asn Ala Pro Val Val Arg Asn Val Ala Gly Asn Asn Lys Gln
 500 505 510
 Val Pro Arg Asp Val Pro Phe Asp Glu Val Phe His Thr Ser Tyr Glu
 515 520 525
 Asp Ser Cys Glu Tyr Leu Ala Arg Thr Leu Lys Arg Thr Lys Asn Tyr
 530 535 540
 Leu Asp Ser Leu Asp Tyr Asp Pro Asn Lys Glu Tyr Pro Pro Leu Ala
 545 550 555 560
 Met Val Tyr Gly Asn Lys Val Pro Thr Val Arg Gly Ala Lys Val Asn
 565 570 575
 Gly Ile Gln Asp Ile Lys Asp Gly Asn Tyr Glu Asp Phe Tyr Tyr Gly
 580 585 590
 Pro Gly Asp Gly Val Val His His Lys Trp Leu Leu Pro Glu Gln Arg
 595 600 605
 Gly Phe Pro Val Val Cys Lys Ile Ala Ser Ser Ser Gly His Val Ser
 610 615 620
 Leu Met Thr Asp Leu Lys Ser Met Ala Lys Ala Phe Ile Ser Ile Val
 625 630 635 640
 Asp Ser Glu Lys Glu Gly Arg Arg Ser Arg Thr Arg Thr Ser Ser
 645 650 655